Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (withdrawn) A method for in vitro detection of acute generalized inflammatory conditions (SIRS), comprising:

isolating sample RNA from a sample of a mammal;

labelling of the sample RNA and/or at least one DNA being a gene or gene fragment specific for SIRS, with a detectable label.

contacting the sample RNA with the DNA under hybridization conditions;

contacting sample RNA representing a control for non-pathologic conditions, with at least one DNA, under hybridization conditions, whereby the DNA is a gene or gene fragment specific for SIRS;

quantitative detection of the label signals of the hybridized sample RNA and control RNA; and

comparing the quantitative data of the label signals in order to determine whether the genes or gene fragments specific for SIRS are more expressed in the sample than in the control, or less.

2. (previously presented) A method for in vitro detection of sepsis and/or sepsis-like conditions,

isolating of sample RNA from a sample of a mammal;

labelling of the sample RNA and/or at least one DNA being a gene or gene fragment specific for sepsis, with a detectable label.

contacting the sample RNA with the DNA under hybridization conditions;

contacting sample RNA representing a control for non-pathologic conditions, with at least one DNA, under hybridization conditions, whereby the DNA is a gene or gene fragment specific for sepsis and/or sepsis-like conditions;

quantitative detection of the label signals of the hybridized sample RNA and control RNA; and

comparing the quantitative data of the label signals in order to determine whether the genes or gene fragments specific for sepsis and/or sepsis-like conditions are more expressed in the sample than in the control, or less.

3. (previously presented) A method for in vitro detection of severe sepsis, comprising:

isolating of sample RNA from a sample of a mammal;

labelling of the sample RNA and/or at least one DNA being a gene or gene fragment specific for severe sepsis, with a detectable label.

contacting the sample RNA with the DNA under hybridization conditions;

contacting sample RNA representing a control for non-pathologic conditions, with at least one DNA, under hybridization conditions, whereby the DNA is a gene or gene fragment specific for severe sepsis;

quantitative detection of the label signals of the hybridized sample RNA and control RNA; and

comparing the quantitative data of the label signals in order to determine whether the genes or gene fragments specific for severe sepsis are more expressed in the sample than in the control, or less.

4. (withdrawn) The method of claim 1, characterized in that the control RNA is hybridized with the DNA before the measurement of the sample RNA and the label signals of the control RNA/DNA-complex is gathered and, if necessary, recorded in form of a calibration curve or table.

5. (withdrawn) The method of claim 1, characterized in that unchanged genes from sample and/or control RNA are used as reference genes for the quantification.

6. (withdrawn) The method of claim 1, characterized in that mRNA is used as sample RNA.

7. (withdrawn) The method of claim 1, characterized in that the DNA is arranged, particularly immobilized, on predetermined areas on a carrier in the form of a microarray.

8. (withdrawn) The method of claim 1, characterized in that the method for early detection by means of differential diagnostics, for control of the clinical and therapeutic progress, for the individual risk evaluation in patients, for the evaluation whether the patient will respond to a specific treatment, as well as for post mortem diagnosis of SIRS and/or sepsis and/or severe sepsis and/or systemic infections and/or septic conditions and/or infections.

9. (withdrawn) The method of claim 1, characterized in that the sample is selected from the following group: body fluids, in particular blood, liquor, urine, ascitic fluid, seminal fluid, saliva, puncture fluid, cell content, or a mixture thereof.

10. (withdrawn) The method of claim 1, characterized in that cell samples are subjected a lytic treatment, if necessary, in order to free their cell contents.

11. (withdrawn) The method of claim 1, characterized in that the mammal is a human.

12. (withdrawn) The method of claim 1, characterized in that the gene or gene segment specific for SIRS is selected from the group consisting of SEQUENCE ID No. III.1 to SEQUECE ID No. III.4168, as well as gene fragments thereof with 5-2000 or more, preferably 20-200, more preferably 20-80 nucleotides.

13. (previously presented) The method of claim 2, characterized in that the gene or gene segment specific for sepsis and/or sepsis-like conditions is selected from the group consisting of SEQUENCE ID No. I.1 to SEQUECE ID No. I.6242, as well as gene fragments thereof with 5-2000 or more, preferably 20-200, more preferably 20-80 nucleotides.

14. (previously presented) The method of claim 3, characterized in that the gene or gene segment specific for severe sepsis is selected from the group consisting of SEQUENCE ID No. II.1 to SEQUECE ID No. II.130, as well as gene fragments thereof with 5-2000 or more, preferably 20-200, more preferably 20-80 nucleotides.

15. (withdrawn) The method of claim 1, characterized in that at least 2 to 100 different cDNAs are used.

16. (withdrawn) The method of claim 1, characterized in that at least 200 different cDNAs are used.

17. (withdrawn) The method of claim 1, characterized in that at least 200 to 500 different cDNAs are used.

18. (withdrawn) The method of claim 1, characterized in that at least 500 to 1000 different cDNAs are used.

19. (withdrawn) The method of claim 1, characterized in that at least 1000 to 2000 different cDNAs are used.

20. (withdrawn) The method of claim 1, characterized in that the cDNA SEQUENCE ID No. III.1 to SEQUECE ID No. III.4168, SEQUENCE ID No. I.1 to SEQUECE ID No. I.6242 and SEQUENCE ID No. II.1 to SEQUECE ID No. II.130 replaced by synthetic analoga as well as peptidonucleic acids.

21. (withdrawn) The method of claim 20, characterized in that the synthetic analoga of the listed genes comprise 5-100, in particular approximately 70, base pairs.

22. (withdrawn) The method of claim 1, characterized in that a radioactive label, in particular ^{32}P, ^{14}C, ^{125}I, ^{155}Eu, ^{33}P or ^{3}H is used as detectable label.

23. (withdrawn) The method of claim 1, characterized in that a non-radioactive label is used as detectable label, in particular a color- or fluorescence label, an enzyme label or immune label, and/or quantum dots or an electrically measurable signal, in particular the change in potential, and/or conductivity and/or capacity by hybridizations.

24. (withdrawn) The method of claim 1, characterized in that the sample RNA and control RNA bear the same label.

25. (withdrawn) The method of claim 1, characterized in that the sample RNA and control RNA bear different labels.

26. (withdrawn) The method of claim 1, characterized in that the immobilized probes bear a label.

27. (withdrawn) The method of claim 1, characterized in that the cDNA probes are immobilized on glass or plastics.

28. (withdrawn) The method of claim 1, characterized in that the individual cDNA molecules are immobilized on the carrier material by means of a covalent binding.

29. (withdrawn) The method of claim 1, characterized in that the individual cDNA molecules are immobilized onto the carrier material by means of adsorption, in particular by means of electrostatic and/or dipole-dipole and/or hydrophobic interactions and/or hydrogen bridges.

30. (withdrawn) A method for in vitro detection of SIRS, comprising:

isolating sample peptides from a sample of a mammal;

labelling of the sample peptides with a detectable label;

contacting the labelled sample peptides with at least one antibody or its binding fragment, whereby the antibody binds a peptide or peptide fragment specific for SIRS;

contacting the labelled control peptides originating from healthy subjects, with at least one antibody or its binding fragment immobilized on a carrier in form of a microarray, whereby the antibody binds a peptide or peptide fragment specific for SIRS;

quantitative detection of the label signals of the sample peptides and the control peptides;

comparing the quantitative data of the label signals in order determine whether the genes or gene fragments specific for SIRS are more expressed in the sample than in the control, or less.

31. (withdrawn) A method for in vitro detection of sepsis and/or sepsis-like conditions, comprising:

isolating sample peptides from a sample of a mammal;

labelling of the sample peptides with a detectable label;

contacting the labelled sample peptides with at least one antibody or its binding fragment, whereby the antibody binds a peptide or peptide fragment specific for sepsis and/or sepsis-like conditions;

contacting the labelled control peptides stemming from healthy subjects, with at least one antibody or its binding fragment immobilized on a carrier in form of a microarray, whereby the antibody binds a peptide or peptide fragment specific for sepsis and/or sepsis-like conditions;

quantitative detection of the label signals of the sample peptides and the control peptides; and

comparing the quantitative data of the label signals in order to be able to determine whether the genes or gene fragments specific for sepsis and/or sepsis-like conditions are more expressed in the sample than in the control, or less.

32. (withdrawn) A method for in vitro detection of severe sepsis, comprising:

isolating sample peptides from a sample of a mammal;

labelling of the sample peptides with a detectable label;

contacting the labelled sample peptides with at least one antibody or its binding fragment, whereby the antibody binds a peptide or peptide fragment specific for severe sepsis;

contacting the labelled control peptides originating from healthy subjects, with at least one antibody or its binding fragment immobilized on a carrier in form of a microarray, whereby the antibody binds a peptide or peptide fragment specific for severe sepsis;

quantitative detection of the label signals of the sample peptides and the control peptides; and

comparing the quantitative data of the label signals in order to determine whether the genes or gene fragments specific for severe sepsis are more expressed in the sample than in the control, or less.

33. (withdrawn) The method of claim 30, characterized in that the antibody is immobilized on an array in form of a microarray.

34. (withdrawn) The method of claim 30, characterized in that it is formed as immunoassay.

35. (withdrawn) The method of claim 30, characterized in that the method is used for early detection by means of differential diagnostics, for control of the clinic and therapeutic progress, for risk evaluation for patients as well as for post mortem diagnosis of SIRS and/or sepsis and/or severe sepsis and/or systemic infections and/or septic conditions and/or infections.

36. (withdrawn) The method of claim 30, characterized in that the sample is selected from the following group: body fluids, in particular blood, liquor, urine, ascitic fluid, seminal fluid, saliva, puncture fluid, cell content, or a mixture thereof.

37. (withdrawn) The method of claim 30, characterized in that cell samples are subjected a lytic treatment, if necessary, in order to free their cell contents.

38. (withdrawn) The method of claim 30, characterized in that the mammal is a human.

39. (withdrawn) The method of claim 30, characterized in that the peptide specific for SIRS is an expression product of a gene or gene fragment selected from the group consisting of SEQUENCE ID No. III.1 to SEQUECE ID No. III.4168, as well as gene fragments thereof with 5-2000 nucleotides or more, preferably 20-200, more preferable 20-80 nucleotides.

40. (withdrawn) The method of claim 31, characterized in that the peptide specific for sepsis and/or sepsis-like conditions is an expression product of a gene or gene fragment selected from the group consisting of SEQUENCE ID No. I.1 to SEQUECE ID No. I.6242, as well as gene fragments thereof with 5-2000 nucleotides or more, preferably 20-200, more preferable 20-80 nucleotides.

41. (withdrawn) The method according to one of claim 32, characterized in that the peptide specific for severe sepsis is an expression product of a gene or gene fragment selected from the group consisting of SEQUENCE ID No. II.1 to SEQUECE ID No. II.130, as well as gene fragments thereof with 5-2000 or more, preferably 20-200, more preferably 20-80 nucleotides.

42. (withdrawn) The method of claim 30, characterized in that at least 2 to 100 different peptides are used.

43. (withdrawn) The method of claim 30, characterized in that at least 200 different peptides are used.

44. (withdrawn) The method of claim 30, characterized in that at least 200 to 500 different peptides are used.

45. (withdrawn) The method of claim 30, characterized in that at least 500 to 1000 different peptides are used.

46. (withdrawn) The method of claim 30, characterized in that at least 1000 to 2000 different peptides are used.

47. (withdrawn) The method of claim 30, characterized in that a radioactive label, in particular ^{32}P, ^{14}C, ^{125}I, ^{155}Eu, ^{33}P or ^{3}H is used as detectable label.

48. (withdrawn) The method of claim 30, characterized in that a non-radioactive label is used as detectable label, in particular a color- or fluorescence label, an enzyme label or immune label, and/or quantum dots or an electrically measurable signal, in particular the change in potential, and/or conductivity and/or capacity by hybridizations.

49. (withdrawn) The method of claim 30, characterized in that the sample peptides and control peptides bear the same label.

50. (withdrawn) The method of claim 30, characterized in that the sample peptides and control peptides bear different labels.

51. (withdrawn) The method of claim 30, characterized in that the probes used are peptides to which labelled antibodies are bound, which cause a change of signal of the labelled antibodies by change of conformation when binding to the sample peptides.

52. (withdrawn) The method of claim 30, characterized in that the peptide probes are immobilized on glass or plastics.

53. (withdrawn) The method of claim 30, characterized in that the individual peptide molecules are immobilized onto the carrier material by means of a covalent binding.

54. (withdrawn) The method of claim 30, characterized in that the individual peptide molecules are immobilized on the carrier material by means of adsorption, in particular by means of electrostatic and/or dipole-dipole and/or hydrophobic interactions and/or hydrogen bridges.

55. (withdrawn) The method of claim 30, characterized in that the individual peptide molecules are detected by means of monoclonal antibodies or their binding fragments.

56. (withdrawn) The method of claim 30, characterized in that the determination of individual peptides by means of immunoassay or precipitation assay is carried out using monoclonal antibodies.

57. (Cancelled)

58. (Cancelled)

59. (Cancelled)